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(without alignments)
2482.410 Million cell updates/sec
                                                                                                                                                                                                                   1 MSGKSFKAGVCPPKKSAQCL.....IEQNTKSPLFMGKVVNPTQK 503
                                                                                                         November 30, 2002, 12:31:03 ; Search time 27 Seconds
                                                                                                                                                                                                                                                                                                                                                            908470
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
                                                                    OM protein . protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A_Geneseq_101002;*
                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                      US-10-025-514-8
                                                                                                                                                                                                Perfect score:
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980_DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980_DAT:*
| SIDS2/gcgdata/geneseq-embl/AA1981_DAT:*
| SIDS2/gcgdata/geneseq-embl/AA1981_DAT:*
| SIDS2/gcgdata/geneseqp-embl/AA1981_DAT:*
| SIDS2/gcgdata/geneseqp-embl/AA1991_DAT:*
| SIDS2/gcgdata/geneseqqgeneseqp-embl/AA1991_DAT:*
| SIDS2/gcgdata/geneseqqgeneseqpeneseqpeneseqqgeneseqqgeneseqpeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqpeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqgeneseqqqeneseqqgeneseqqqeneseqqqeneseqqqeneseqqqeneseqq

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	SLAPI fusion prote Sequence of human Predominant form o Human alphal-anti- TAPI fusion protei Human alpha-1-tryp Amino acid sequenc Human alphal-antit Human alphal-antit Human alphal-antit
SUMMARIES	AAU99881 AAP40133 AAP94664 AAY26925 AAU99882 AAR71969 AAR78890 AAR36101 AAB36101
DB	23 23 23 21 21 21
Query Match Length DB	503 418 418 418 580 418 418 417
& Query Match	100.00 76.7 76.7 76.7 76.8 76.4 76.4 76.4
Score	20052.5 20052.5 20052.5 20052.5 20043.5 20043.5 20043.5
Result No.	10843310 10884310 1088

27-JUN-2002

118 10 AAPO0128 552 2 AAU99883 552 2 3 AAU99883 560 23 AAU99885 560 23 AAU99885 418 6 AAP50021 418 6 AAP50021 418 6 AAP50021 418 6 AAP50021 304 23 AAU99873 304 12 AAP50802 305 41 AAP50802 305 41 AAP50802 306 16 AAP50802 307 4 AAP50110 308 11 AAP50110 308 10 AAP50111 309 1 AAP50132 309 1 AAP50132 309 1 AAP50133 48 6 AAP50133 49 1 AAP60333 40 1 AAP60333 40 1 AAP60333 41 6 AAP60333 42 20 AAY44201 43 4 16 AAP60333 44 16 AAP60333 45 4 16 AAP60333 46 6 AAP60333 47 1 AAP60333 48 6 AAP60333 48 6 AAP60333 49 10 AAP60333 40 10 AAP60333 41 10 AAP60333 42 10 AAP60333 43 10 AAP60333 44 16 AAP60333 45 10 AAP60333 46 10 AAP60333 47 10 AAP60333 48 10 AAP60333 49 11 AAR60333 40 10 AAP60333 40 10 AAP60333 40 10 AAP60333 40 10 AAP60333 40 10 AAP60333 40 10 AAP60333 40 10 AAP60333	Sequence encoded brSLAP1 fusion prote NTAP1 fusion prote rTAP1 fusion prote Sequence of alpha- Alpha-1 antirrypsi Sequence of human Mature protein seq Human alpha-1-anti Sequence encoded b Alpha-1-antirrypsi Human alpha-1-anti Human alpha-1-anti Human alpha-1-anti Human alpha-1-anti Human alpha-1-anti Human alpha-1-anti Ileu358] alphal-an [Ile358] alphal-an [Ile358] alphal-an [Ile358] alphal-an Alpha-1-antitrypsi (Gly358] alphal-an Alpha-1-antitrypsi (Gly358] alphal-an Alpha-1-antitrypsi Sequence of the pr Alpha-1 antitrypsi Alpha-1 antitrypsi	Sequence of fusion Sequence of fusion Human alpha-1-anti Sequence of human (Ala357, Arg358) A [delta 1-5][Arg358
	AAP9012 AAU9988 AAU9988 AAP5021 AAF5021 AAF50273 AAF50573 AAF6736 AAF6736 AAF6736 AAF6736 AAF6736 AAF67712 AAF67713 AAF67713 AAF67713 AAF67713 AAF67713 AAF67713 AAF67713 AAF67713 AAF67736	989
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	000000000000000000000000000000000000000	15531
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ALIGNMENTS

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malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; tumour anglogenesis; osteoporosis; Paget's disease; glomerulonephritis; scleroderma; hypertension.
                                                                                                                                                                                                                                                                                                       /note= "Linker amino acid"
110..503
/note= "Amino acids 1-394 of human AAT protein"
                                                                                                                                                                                                                                                                                  /note= "Amino acids 1-107 of SLPI"
                                                                                                           Alzheimer's disease; SLAP1; fusionprotein;
         AAU99881 standard; Protein; 503 AA.
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                               (first entry)
                                                                                    SLAP1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                         WO200250287-A2
                                                                                                                                                                                                                 Homo sapiens.
                                                            07-OCT-2002
                                                                                                                                                                                                                               Synthetic.
                                    AAU99881;
                                                                                                                                                                                                                                                        Key
Region
                                                                                                                                                                                                                                                                                              Region
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AAU99881
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216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                              Sequence of human alpha-1-antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1A; 48pp; English.
                                                                                                                                                                                     AAP40133 standard; Protein; 418 AA.
                                                      481 FLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                         481 FLMIEQNTKSPLFMGKVVNPTQK 503
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25..418
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82US-0409183.
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                                                                                                                                                                                                                                                               16-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1984-077108/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAWA/) KAWASAKI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-APR-1983;
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-1984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP103409-A.
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                                                                                                                                                                                                                              AAP40133;
                                                                                                                                                                                                                                                                                                                                                               therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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                                                              δλ
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                                                                                                                                                                                                                                                                                                                                                   processe inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion and a second protease inhibitor or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion protein of the invention inhibitor of protease activity. The fusion protein of the invention inhibitor of protease activity associated with a disorder is useful for inhibiting protease activity associated with a disorder is useful for inhibiting protease activity special or its active for treating an individual suffering from or at risk for a disease or for treating an individual suffering from or at risk for a disease or for treating dermatological diseases such as atopic dermatitis, eczema for treating herpes infection, corneal or epideral infection, and for treating herpes infection, corneal or epideral infection, and for treating wounds, sepsis, rheumatoid arthritis, periodontal disease, non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tamour metastaals and tumour angiogenesis, gastric ulceration, corteand pactual infection, Alzheimer's disease, hypertension and muscular bacterial infection, Alzheimer's disease, hypertension and muscular chartening in the present sequence represents the SLAPI fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                            Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 FFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THDEILEGLNFNLTEIPEAQIHEGFOELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKAMEDPQGDAAQKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel fusion protein comprising a first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 2675; DB 23;
100.0%; Pred. No. 1.4e-198;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                Example 1; Page 74-76; 134pp; English.
                                                                                                                              Pemberton P;
18-DEC-2001; 2001WO-US49256.
                                   18-DEC-2000; 2000US-256699P.
20-NOV-2001; 2001US-331966P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 503; Conservative
                                                                                           (ARRI-) ARRIVA PHARM INC.
                                                                                                                                Barr PJ, Gibson HL,
                                                                                                                                                                   2002-500631/53.
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                                                                                                                                                                                     N-PSDB; ABK88022.
                                                                                                                                                                                                                                                                                   inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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96 GMCGKSCVSPVKAMEDPQCDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extra:chromosomal element for replication in yeast - with yeast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease inhibitor; enzyme; proteolysis inhibitor; emphysema;
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New in the patent are unglycosylated polypeptides having the amino acid sequence of a mammalian alpha-1-antitrypsin (AT). Also claimed is the prodon of polypeptides having the protease-inhibiting activity of a mammalian AT. A culture of microorganisms is grown such as fungi or yeast, esp. Saccharomyces cerevisiae GK 100, which are transformed with a BOMA transfer vector 2-mu plasmid, plasmid CATI or plasmid HAT4, contg. as egement encoding the mammalian AT. The unglycosylated polypeptides are activity in mammals, and for treating AT deficiency, esp. for replacing AT which has been inactivated (oxidised) by tobacco or other smoke. In the given example plasmid HAT4 comprises the yeast promoter, an ATGGAGGATCC adapter, the hAT gene and the yeast TPI terminator inserted
                                                                                                                                                                                                                                                                                                                                                                                                                      Human alpha-1-trypsin (hAT); anti-AT antibodies; proteolytic activity;
AT deficiency; Saccharomyces cerevisiae GK 100; 2-mu plasmid DNA; CATI;
plasmid HAT4; yeast TPI promoter; yeast TPI terminator;
276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                      336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                             396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                    Predominant form of human alpha-1-antitrypsin as encoded by cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New alpha-1-antitrypsin polypeptide(s) -
produced by recombinant DNA techniques esp. using yeast host
                                                                                                                                                                                                         456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                         82EP-0201179, US-408099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83EP-0201179
                                                                                                                                                                                                                                                                                                                                                               28-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawasaki GH, Woodbury RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..118
119..418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1989-062651/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN91077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989
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into plasmid C1/1, which contains the entire 2-mu DNA from S. cerevisiae. S. cerevisiae GK100 transformed with HAT4 produces soluble protein with an hAT content of 2-3% when grown on a medium contg. 6% glucose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; alpha-1-ant1-trypsin; transgenic plant; monocotyledon; variant; glycosylation; serine protease; inhibitor; neutrophil; elastase; trypsin; cathepsin G; thrombin; pulmonary tissue; protease damage; septic shock; pulmonary emphysema; cystic fibrosis; rheumatism; recombinant; virus contamination; immunogenicity; ss.
                                                                                                                              96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                               156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                              216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                         396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                                                                   DB 10; Length 418;
                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note" "putative glycosylation site"
                                                                              76.7%; Score 2052.5; DB 1(
97.8%; Pred. No. 1.7e-150;
tive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "putative active site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alphal-anti-trypsin type Ml protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label = mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY26925 standard; Protein; 418 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                    Matches 399; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382..387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418
                                                                                          Similarity
                                                      418 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-AUG-1999
                                                     Sequence
                                                                              Query Match
                                                                                            Best Local
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This invention relates to a novel fusion protein comprising a first

protease inhibitor comprising an alphal-antitrypsin or its functionally

active portion and a second protease inhibitor or its functionally

cative protein. The fusion proteins of the invention may act as an

active protein. The fusion protein of the invention

inhibitor of protease activity. The fusion protein of the invention

consistent of protease activity associated with a disorder

such as emphysema, asthma, chronic obstructive pulmonary disease,

such as emphysema, asthma, chronic obstructive pulmonary disease,

cystic fibrosis, othis media, othis external or HIV infection, or

cystic fibrosis, othis media, othis activity. The proteins are useful

closureder involving unwanted protease activity. The proteins are useful

consistenting dermatological diseases such as atopic dermatitis, eczema

con psoriasis, in inflammatory responses to viral infection, and for

creating hereps infection, corneal or epidermal ulceration, chronic

creating herestasis and tumour angiogenesis, spartic ulceration,

conceptorosis, paget's disease, glomerulonephritis, scleroderma, malaria,

be acterial infection, Alzheimer's disease, hypertension and muscular

chastrophy, The present sequence represents the TAPI fusion protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                            malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; Paget's disease; scleroderma; glomerulonephritis; hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 RDLKCC---MGMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 76.5%; Score 2045.5; DB 23; Length 580; Local Similarity 95.9%; Pred. No. 8.9e-150; nes 401; Conservative 2; Mismatches 12; Indels 3;
                                                                                                                                                                                                                                                                                                                                              /note= "Linker methionine"
187..580
/note= "Amino acids 1-394 of human AAT"
                                                                                                                                                                                                                                                                                           2..185
/note= "Human TIMP-1 amino acids 1-184"
                                 TAP1; Alzheimer's disease; tumour anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 79-82; 134pp; English.
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pemberton P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-2000; 2000US-256699P.
20-NOV-2001; 2001US-331966P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2001; 2001WO-US49256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ARRI-) ARRIVA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barr PJ, Gibson HL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-500631/53.
TAP1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABK88023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200250287-A2.
                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-2002.
                                                                                                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibitor
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                                                                                                                                                                                                                                                                                                                                                       This sequence represents the coding region of the human alpha-1-antitrypsin (AT) gene. The invention relates to the production of AT in plant cells, especially monocotyledonous plants. Also produced are variants of altered. AT inhibits serine proteases, specifically neutrophil elastase (but also trypsin, cathepsin G, thrombin etc.) so protect pulmonary tissue against protease damage. AT are used to treat AT-deficiency conditions, particularly pulmonary emphysema, cystic fibrosis, septic of AT results in a product without risk of (sub)viral contamination. The recombinant AT had good activity and is stable, with low immunogenicity (associated with glycosylation patterns similar to the native protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 FNIQHCKKLSSWYLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Production of alphal-antitrypsin, and its variants, in cells of monocotyledonous plants, useful as serine protease inhibitors for therapy, e.g. of emphysema, in cosmetics and as reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.7%; Score 2052.5; DB 20; Length 418; 97.8%; Pred. No. 1.7e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 AAGAMELEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                 Gruber V, Olagnier B, Bournat P, Theisen M, Merot B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.7e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU99882 standard; Protein; 580 AA.
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                                                                                               (MERI-) MERISTEM THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 1; 67pp; French.
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               99WO-FR00195
                                                          98FR-0001089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399; Conservative
                                                                                                                                                                                    WPI: 1999-469334/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 AA;
                                                                                                                                                                                                           N-PSDB; AAX83548
                 29-JAN-1999;
                                                            30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU99882;
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AAU99882
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146 LYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGF 205
                                 206 QELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQ 265
                                                                  326 KVPWMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFL 385
                                                                                                              386 ENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKA 445
                                                                                                                                               446 VLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                Human alphal-antitrypsin (al-AT) cDNA sequence - can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of human alpha-1-antitrypsin encoded by an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davie EW, Kurachi K, Thirumalachary C,
                                                                                                                                                                                                                                                                                                     Alpha-1-trypsin; protease-inhibitor.
                                                                                                                                                                                                                                                                                                                                                  1..24
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
                                                                                                                                                                                                                                AAR71969 standard; Protein; 418 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig.1; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          87US-0022543.
87US-0133190.
88US-0246912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WASH-) WASHINGTON RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                          82US-0380310
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84US-0638980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0398288
91US-0666450
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                                                                                                                                                                                                                                                                   18-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the expression of al-AT
                                                                                                                                                                                                                                                                                    Human alpha-1-trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-130740/17.
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                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                       US5399684-A.
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cDNA clone is given in AAR71969. Expression of the cDNA in host cell transformants allowed production of recombinant alpha-1-antitrypsin.
                                                                                                96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                         156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                      216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                         FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                    396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                           76.4%; Score 2043.5; DB 16; Length 418; 97.5%; Pred. No. 8.2e-150; 1ve 2; Mismatches 5; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human alpha-1-antitrypsin; ATR-1; antibody; ATR-1 deficiency.
                                                                                                                                                                                                                                                                                                                                                              456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                           Davie EW, Kurachi K, Thirumalachary C, Woo SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the alpha-1-antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW56709 standard; Protein; 418 AA.
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87US-0022543.
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89US-0398288.
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                                                  Ouery Match
Best Local Similarity 97.59
Matches 398; Conservative
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                                  418 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1982;
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                                  Seguence
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16-FEB-2001
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           15-DEC-1987
03-MAR-1987
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                                                                                           This is the amino acid sequence of the novel human alpha-1-antitrypsin
                                                                                                   (ATR-1) protein. Its products are useful for producing recombinant ATR-1 polypeptides, which can be used to prepare antibodies for adetecting ATR-1 variants in the blood, as ligands in assays for ATR-1, and to treat ATR-1 deficiency.
                                                                                                                                                                                                                                                                                                                                       276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                                                                                                                                    FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                              156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                                                                                                                           96 GWGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLXRQLAHQSN 155
                                                                                                                                                                                                                                                       14 GLC---CLVPVSLAEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 70
                                                                                                                                                                                                               3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alphal-antitrypsin; neutrophil elastase inhibitor; human;
chronic obstructive pulmonary emphysema; infantile liver cirrhosis.
                                                                                                                                                                                                                                                                                                                                                                                    76.4%; Score 2043.5; DB 19; Length 418; 97.5%; Pred. No. 8.2e-150; tive 2; Mismatches 5; Indels 3;
                                    DNA encoding alpha-1 anti-trypsin - useful for, e.g. producing recombinant alpha-1 anti-trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human alphal-antitrypsin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78890 standard; Protein; 418 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0009581.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82US-0380810.
84US-0638980.
                                                                          Claim 1; Fig 1; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-2000 (first entry)
                                                                                                                                                                                                                 398; Conservative
                                                                                                                                                                                                         Local Similarity
         WPI; 1998-239214/21
                                                                                                                                                                       418 AA;
                    N-PSDB; AAV28471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1982;
07-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS6025161-A.
                                                                                                                                                                         Sequence
                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             336
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sequence. Alphal-antitrypsin is an important protease inhibitor, the major function of which is to inhibit neutrophil elastase. Low levels of alphal-antitrypsin in the blood are associated with chronic obstructive pulmonary emphysema and infantile liver cirrhosis. A vector comprising a mammalian alphal-antitrypsin DNA sequence that hybridises to human alphal-antitrypsin cDNA can be introduced into a host cell in a method for the production of alphal-antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDXVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 GKIYDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 GMCGKSCVSPVKAMEDPQGDAAQKIDISHHDQDHPIFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 GLC---CLVPVSLAEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the human alphal-antitrypsin amino acid
                                                                                                                                                                                                                                                                                                                                           preparing alphal-antitrypsin for inhibiting neutrophil elastase involves transfecting host cell with vector comprising alphal-antitrypsin DNA sequence that hybridizes to human alphal-antitrypsin cDNA, or its complement .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                            Woo SLC, Thirumalachary C, Kurachi K, Davie EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 76.4%; Score 2043.5; DB 21
Best Local Similarity 97.5%; Pred. No. 8.2e-150;
Matches 398; Conservative 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36101 standard; Peptide; 417 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 16pp; English.
                                          88US-0246912.
89US-0398288.
91US-0666450.
                                                                                                                                                                                       (WASH-) WASHINGTON RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
87US-0022543.
87US-0133190.
                                                                                                                92US-0979556.
                                                                                                                                            93US-0086442.
                                                                                                                                                                                                                                                                                      WPI: 2000-181811/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 AA;
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                                                                      22-AUG-1989;
11-MAR-1991;
18-NOV-1992;
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                                           Human; alphal-proteinase inhibitor; periodontain; antiinflammatory;
antibacterial; amidolytic; alpha_l-proteinase inhibitor; periodontitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is given in a specification relating to novel oral bacterial polypeptide referred to as periodontain. The polypeptide amidolytic activity for cleavage of denatured polypeptides and non-denatured serpin polypeptides. It has amidolytic activity for cleavage of a non-denatured human alpha_l-proteinase inhibitor at a inhibiting the peptidase activity and periodontain is useful for reactive site loop regoin of the inhibitor. Periodontain is useful for tooth attachment and periodontal pocket formation, and for reducing growth of bacteria, preferably P. gingivalis in vitro or in vivo. It is useful for protecting an animal from a disease caused by gingivalis and for treating periodontal diseases, including gingivitis and periodontitis.
                                                                                                                                                                                                                                                                                                                                                                                                              Novel oral bacterial periodontain polypeptide for treating periodontal diseases, has amidolytic activity for cleavage of non-denatured human alphal-proteinase inhibitor at reactive site loop region of inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITFPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNOP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276 GKIVDLVKELDRDTVFALNNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 FNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.4%; Score 2042.5; DB 21; Length 417; 97.3%; Pred. No. 9.8e-150; tive 3; Mismatches 5; Indels 3;
                                                                                                                                                                                                                                                                   (UYGE-) UNIV GEORGIA RES FOUND INC.
               Human alphal-proteinase inhibitor.
                                                                                                                                                                                                                                                                                                                                                         Nelson D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 4; 55pp; English.
                                                                                                                                                                                                        20-APR-2000; 2000WO-US10574.
                                                                                                                                                                                                                                            99US-0130436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 97.3%
Matches 397; Conservative
                                                                                                                                                                                                                                                                                                                                                      Potempa J,
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-679600/66.
                                                                                                                                                                                                                                                                                        (TRAV/) TRAVIS J.
(POTE/) POTEMPA J.
(NELS/) NELSON D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 AA;
                                                                                                                                            WO200063394-A2.
                                                                                                             Homo saplens.
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                                                                                                                                                                             26-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                    Travis J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
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This sequence represents the human alphal-antitrypsin protein. Antitrypsin is a serine protease inhibitor, and is used in the present invention as a nitric oxide (NO) synthesia suppressor. The invention relates to the treatment of diseases through the administration of an agent (e.g. antitrypsin) that suppresses nitric oxide synthesia. The method can be used in human or veterinary medicine for treating tubulointerstitial disease, acute pencreatitis, acute respiratory failure of distress syndrome, age associated memory impairment, AIDS, airway contamination, Alzheimer's and Parkinson's disease, amyctrophic lateral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Intrammentou, Alzerelmer, a sume relatations a usease, amyorocopius satematical solutions at the statematical solutions and attempts at the statement and a statement a statement and a statement a statement and a statement a statem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPhal-antitrypsin; human; serine protease inhibitor; nitric oxide; NO; synthesis suppressor; tubulointersitital disease; pancreatitis; respiratory disease; Albi; Alzheimer's disease; parkinson's disease; parkinson's disease; parkinson's disease; cerebral ischeamia; Alzheimer's disease; carcinogenesis; cerebral ischeamia; liver disease; lung disease; ottinis media; heart failure; diabetes; dysmenorrhoea; endotoxic shock; glaucoma; chinese restaurant syndrome; gastritis; hot dog headache; hypertension; inflammatory disease; liver disease; migraine; multiple sclarosis; neurodegenerative disease; orthopaedic disease; protozoan infection; sickle cell anaemia; stroke; systemic lupus erythematosus.
Treating disease e.g. autoimmune disease and hypertension by administering agent which inhibits nitric oxide synthesis and e.g. alphal-antitrypsin -
                                                                                         456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                          Alphal-antitrypsin; human; serine protease inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human alphal-antitrypsin protein sequence.
                                                                                                                                                                                                                                                                                                         AAB26705 standard; protein; 417 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYTE-) UNIV TECHNOLOGY CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-2001 (first entry)
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29-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                            AAB26705;
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                                                                                                                                                                                                                                                    RESULT 10
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diseases, liver cirrhosis, liver disease, Lyme neuroborreliosis, migraine, multiple sclerosis, myocardial infarction, neonatal and paediatric respiratory failure, nephrotoxicity, neurodegenerative disease, orthopaedic disease, osteoarthritis, oxidant stress, paediatric pulmonary disease, pleural inflammation, preclampsia, primary ciliary dyskinesia, primary pulmonary hypertension, protozoan infections, retinal disease, septic shock, sickle cell anaemia, rheumatoid arthritis, stroke, systemic lupus erythematosus, traumatic brain injury, tumour progression and vascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                336 FNIQHCKKLSSWVLLMKYLGNATALFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKIVDLVKELDRDTVFALVNY1FFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
                                                                                                                                                                                                                  96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
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                                                                                                                                                                                                                                                                                    216 DSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQ 275
                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                                                                                                                                                                                                                 76.4%; Score 2042.5; DB 21; Length 417; 97.3%; Pred. No. 9.8e-150; tive 3; Mismatches 5; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Emphysema; lung disorder; therapy; pulmonary disease; respiratory distress syndrome; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence encoded by alpha-1-antitrypsin (AT) cDNA.
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/label= signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO-) ZYMOGENETICS INC.
                                                                                                                                                                                               397; Conservative
                                                                                                                                                                                    Local Similarity
                                                                                                                                             417 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-DEC-1986;
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                                                                                                                                                Sequence
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malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; ottiss external; HV; psoriasis; eczema; buman immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes, ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; paget's disease; scleroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 HLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 FNIQHCKKLSSWYLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 GKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGM 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 GMCGKSCVSPVKAMEDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSN 155
                                                                                                                                                                                                                                                                                                                                                                                                                                      156 STNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                                                                                                                                              The inventors claim a method for the prodn. in yeast of recombinant human AT. The prefd. plasmid is HAT4 which has the TPI promoter, ATGGAGGATCC adaptor, human AT gene (from the BamHI site) and TPI terminator inserted into C1/1. The recombinant AT may be useful for treatment of a genetic AT deficiency and other diseased states related to inadequate levels of AT; dosage is pref. 0.5-10.0 g/week
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or
or
                                                                                                                                                                                                                                                                                                               Score 2040.5; DB 10; Length 418;
Pred. No. 1.4e-149;
6; Mismatches 4; Indels 3;
                                                                        Prepn. of polypeptide with human alpha-1-antitrypsin activity for treating emphysema, chronic obstructive pulmonary disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456 AAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rSLAP1; Alzheimer's disease; tumour angiogenesis;
                                                                                                                                       Disclosure; Fig 1A and Fig 1B; 13pp; English.
                                                                                                           adult respiratory distress syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU99884 standard; Protein; 503 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glomerulonephritis; hypertension.
                                                                                                                                                                                                                                                                                                                         76.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                     N-PSDB; AAN90341, AAN97127
                                                                                                                                                                                                                                                                                                                                                          395; Conservative
         Kawasaki GH, Woodbury R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rSLAP1 fusion protein.
                                       WPI; 1989-220174/30.
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                               418 AA;
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Con as emphysema, others activity associated with a disorder cystic fibrosis, others media, others external or HIV infection, or cystic fibrosis, others are useful for treating demandial suffering from or at risk for a disease or for treating demandiogical diseases such as atopic dermatitis, eczema psoriasis, in inflammatory responses to viral infection, and for contenting wounds, sepsis, rheumatoid arthritis, periodontal disease, two when infection, and for the content metastasis and theumour anglogenesis, astric ulceration, chronic conhealing wounds, sepsis, rheumatoid arthritis, scleroderma, malaria, bacterial infection, Alsheimer's disease, hypertension and muscular distances.
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                                                                                                                                  397..503
/note= "Amino acids 1-107 of human AAT"
                                                                              /note= "Human AAT amino acids 1-394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 76.1%; Score 2035; DB 23;
Similarity 100.0%; Pred. No. 4.8e-149;
95; Conservative 0; Mismatches 0;
                                                                                                     /note= "Linker methionine" 397..503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 90-91; 134pp; English.
                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        Pemberton P;
                                                                                                                                                                                                                                                18-DEC-2001; 2001WO-US49256.
                                                                                                                                                                                                                                                                              18-DEC-2000; 2000US-256699P.
20-NOV-2001; 2001US-331966P.
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Matches 395; Conservative
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Homo sapiens.
Synthetic.
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NTAP1; Alzheimer's disease; tumour angiogenesis; malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; paget's disease; scleroderma; glomerulonephritis; hypertension.
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349 LLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDL 408
                                                                                                                                                                                      409 KSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMS 468
                                                                                                                                                                                                                         'note= "Human TIMP-1 amino acids 1-184"
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                                                                                                                                                                                                                                                                                                                                   361 IPPEVKFNKFFVFLMIEQNTKSPLFMGKVVNPTQK 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU99883 standard; Protein; 522 AA.
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is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema or preating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodoinal disease, tunnour metastasis and tunnour angiogenesis, astrict ulceration, malaria, cateoporosis, paget's disease, appearulonephritis, scheroderma, malaria, destrophy The present sequence represents the WTAPI fusion protein of the invention.
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                                                                                                                                                                                                                                                                                   76.1%; Score 2035; DB 23; Length 522; 100.0%; Pred. No. 5e-149; Indels 0; Mismatches 0; Indels 0;
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Synthetic.
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This invention relates to a novel fusion protein comprising a first

CC active portion and a second protease inhibitor or its functionally

CC active portion and a second protease inhibitor or its functionally

CC active protein. The fusion proteins of the invention may act as an

CC active protein. The fusion protein of the invention

CC is useful for inhibiting protease activity associated with a disorder

CS such as emphysema, asthma, chronic obstructive pulmonary disease,

CS such as emphysema, asthma, chronic obstructive pulmonary disease,

CC cystic fibrosis, ofitis madia, ofitis axternal or HIV infection, or

CC for treating an individual suffering from or at risk for a disease or

CC for treating dermatological diseases such as atopic dermatitis, eczema

CC and psoriasis, in inflammatory responses to viral infection, and for

CC treating herpes infection, corneal or epidermal ulceration, chronic

CC cnon-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,

CC tumour metastasis and tumour anglogenesis, asstric ulceration,

CC dystrophy, The present sequence represents the rN-TAPI fusion protein of

CC dystrophy. The present sequence represents the rN-TAPI fusion protein of
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                                                               /note= "Amino acids 1-126 of human TIMP-1"
/note= "Human AAT amino acids 1-394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.1%; Score 2035; DB 23
100.0%; Pred. No. 5e-149;
tive 0; Mismatches 0
                  /note= "Linker methionine" 397..522
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                                                                                                                                                                                                                                                                                               Pemberton P;
                                                                                                                                                                                                          18-DEC-2000; 2000US-256699P.
20-NOV-2001; 2001US-331966P.
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for treating dermatological diseases such as atopic dermatitis, eczema and psorlasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angilogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular the invention.

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rTAP1; Alzhelmer's disease; tumour angiogenesis; malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; ottiss media; ottiss external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsia; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; Paget's disease; scleroderma; glomerulonephritis; hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
241 LLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDL 300
                      409 KSVLGOLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMS 468
                                    397..580
/note= "Amino acids 1-184 of human TIMP-1"
                                                                                                                                                                                                                                                                                                                                                                                                               'note "Human AAT amino acids 1-394"
                                                                      469 IPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 503
                                                                                    361 IPPEVKENKPEVELMIEQNTKSPLEMGKVVNPTQK 395
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                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                      AAU99889 standard; Protein; 580 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 94; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pemberton P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-DEC-2001; 2001WO-US49256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2000; 2000US-256699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2001; 2001US-331966P.
                                                                                                                                                                                                      07-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ARRI-) ARRIVA PHARM INC.
                                                                                                                                                                                                                              rTAP1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barr PJ, Glbson HL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-500631/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABK88026.
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                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                 AAU99889;
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This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, ottiis media, ottiis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful

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                                                                                                                                                                                                                                                       169 AFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLF 228
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                                                                                                                                                                                                                                                                                                                         LSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRD 288
                                                                                                                                                                                                                                                                                                                                                              TVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWV 348
                                                                                                                                                                                                                                                                                                                                                                                                               349 LLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDL 408
                                                                                                                                                                                                                                                                                                                                                                                                                              409 KSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMS 468
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tive 0; Mismatches 0;
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